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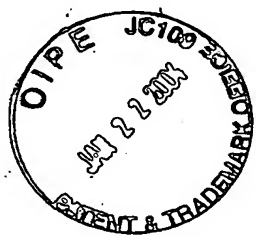
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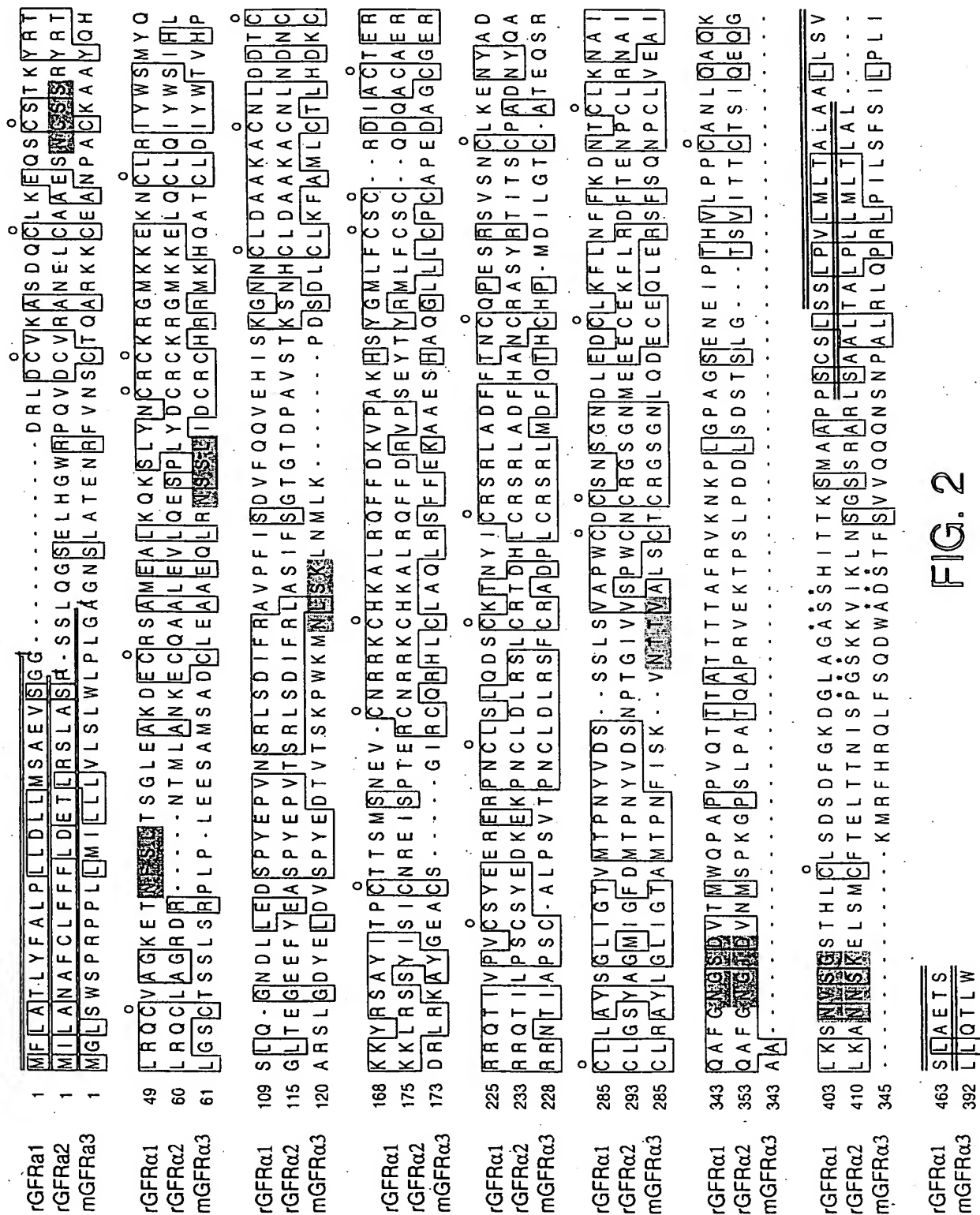
1 GAATTTGGCC CTCGAGGCCA AGAATTCCGC ACAGGGCGG GCGCCAGCG CAGGCAGAGC GCTGTGCGAT CCGGGCGTC CACCCGCCAT GGGGCTCTCC
CTTAAACCGG GAGCTCCGGT TCTTAAGCCG TGCTCCCGC CGCGGTCGC GTCCGTCTCG CGACAGCGTA GGGCCCGCAG GTGGCGGTA CCCCAGAGG
Me tGlyLeuSer
101 TGGAGCCCGC GACCTCCACT GCTGATGATC CTGCTACTGG TGCTGTCTGT GTGGCTGCCA CTTGGAGCAG GAAACTCCCT TGCCACACAG AACAGGTTTG
ACCTCGGGC CTGGAGGTGA CGACTACTAG GACGATGACC ACAGAGCAA CACCGACGGT GAACCTCGTC CTTTGGAGGA ACGGTGTCTC TTGTCCAAAC
5 TrpSerProA rgProProLe uLeuMetIle uLeuLeuV alLeuSerLe uTrpLeuPro LeuGlyAlaG lyAsnSerLe uAlaThrGlu AsnArgPheVal
201 TGAACAGCTG TACCCAGGCC AGAAAGAAAT GCGAGGCTAA TCCTCGCTTG CAGGCTGCCT ACCAGCACCT GGGCTCCTGC ACCTCCAGTT TAAGCAGGCC
ACTTGTGAC ATGGGTCCGG TCTTTCTTTA CGCTCCGATT AGGCGAACG TTCCGACGGA TGGTCGTGGA CCGAGGACG TGGAGGTCAA ATTCTGTCGG
39 AsnSerCy sThrGlnAla ArgLysLysC ysGluAlaAs nProAlaCys LysAlaAlaT yrGlnHisLe uGlySerCys ThrSerSerL euSerArgPro
301 GCTGCCCTTA GAGGAGTCTG CCATGTCTGC AGACTGCCTA GAGGAGCAG AACAACTCAG GAACAGCTCT CTGATAGACT GCAGGTGCCA TCGGCGCATG
CGACGGGAAT CTCCTCAGAC GGTACAGACG TCTGACGGAT TCTCGTCGTC TTGTTGAGTC CTTGTGCGA GACTATCTGA CGTCCACGGT AGCCGCGTAC
72 LeuProLeu GluGluSerA laMetSerAl aAspCysLeu GluAlaAlaG luGlnLeuAr gAsnSerSer LeulleAspC ysArgCysHi sArgArgMet
401 AAGCACCAAG CTACCTGTCT GGACATTTAT TGGACCGTTC ACCCTGCCG AAGCCCTTGT GACTACGAGT TGGATGTCTC ACCCTATGAA GACACAGTGA
TTCTGTGTTT GATGGACAGA CCTGTAATA ACCTGGCAAG TGGACCGGC TTCCGGAACCA CTGATGCTCA ACCTACAGAG TGGGATACCT CTGTGTCTACT
105 LysHisGlnA laThrCysLe uAspIleTyr TrpThrValH isProAlaAr gSerLeuGly AspTyrGluL euAspValSe rProTyrGlu AspThrValThr
501 CCAGCAAACC CTGGAANAATG AATCTTAGCA AGTTGAACAT GCTCAAACCA GACTCGGACC TCTGCCTCAA ATTTGCTATG CTGTGTACTC TTCACGACAA
GGTCGTTTGG GACCTTTTAC TTAGAATCGT TCAACTTGTA CGAGTTTGGT CTGAGCCTGG AGACGGAGTT TAAACGATAC GACACATGAG AAGTGTCTGT
139 SerLysPr oTrpLysMet AsnLeuSerL ysLeuAsnMe tLeuLysPro AspSerAspL euCysLeuL ysPheAlaMet LeuCysThrL euHisAspLys
601 GTGTGACCGC CTGCGCAAGG CCTACGGGA GGCATGCTCA GGTATCCGT GCCAGCGCA CCTCTGCCTA GCTCCTTCTT TGAGAAGGCA
CACACTGGCG GACGCGTTCC GGATGCCCTC CGTACGAGT CCCTAGGCGA CGGTCCGGT GGAGACGGAT CCGGTGCGAG CGAGGAAGAA ACTCTTCCGT
172 CysAspArg LeuArgLysA laTyrGlyG l ualaCysSer GlyIleArgC ysGlnArgHi sLeuCysLeu AlaGlnLeuA rgSerPhePh eGluLysAla
701 GCAGAGTCCC ACGTCAAGG TCTGCTGCTG TGTCCTGTG CACCAAGA TGCGGGCTGT GGGAGCGGC GGCCTAACAC CATCGCCCC AGTTGCGCCC
CGTCTCAGG TGGAGTCCC AGACGACGAC ACAGGGACAC GTGTCTTCT GTGCTTCTT ACGCCCGACA CCCCTCGCG CCGCATTTGT GTAGCGGGG TCAACGCGG
205 AlaGluSerH isAlaGlnG l yLeuLeuLeu CysProCysA laProGluAs pAlaGlyCys GlyGluArgA rgArgAsnTh rIleAlaPro SerCysAlaLeu
801 TGCTTCTGT AACCCCAAT TGCTTGGATC TGCGGAGCTT CTGCGCTGCG GACCTTTGT GCAGATCAG CCTGATGGAC TTCCAGACCC ACTGTCTATCC
ACGAAGACA TTGGGGTTA ACGGACCTAG ACGCTCGAA GACGGCACGC CTGGGAACA CGTCTAGTGC GGAATCTGG AAGTCTGGG TGACAGTAGG
239 ProSerVa lThrProAsn CysLeuAspL euArgSerPh eCysArgAla AspProLeuC ysArgSerAr gLeuMetAsp PheGlnThrH isCysHisPro
901 TATGACATC CTTGGGACTT GTGCAACTGA GCAGTCCAGA TGCTTCGGG CATACCTGG GCTGATTGG ACTGCCATGA CCCCAACTT CATCAGCAAG
ATACCTGTAG GAACCTGAA CACGTTGACT CGTCAGGTCT ACAGACGCC GTATGGACCC CGACTAACCC TGACGGTACT GGGGTTTGA GTAGTCGTTT
272 MetAspIle LeuGlyThrC ysAlaThrG l uGlnSerArg CysLeuArgA laTyrLeuG l yLeuIleGly ThrAlaMetT hrProAsnPh eIleSerLys

FIG. 1A



1001 GTCAACACTA CTGTTGCCTT AAGCTGCACC TGCCGAGGCA GCGGCAACCT ACAGGACGAG TGTGAACAGC TGTCTCCCAG AACCCCTGCC
CAGTTGTGAT GACAACGGAA TTTCGACGTGG ACGGCTCCGT CGCCGTTGGA TGTCCTGCTC ACACCTGTGC ACCTTTCCAG GAAGAGGGTC TTGGGACGG
305 ValAsnThr hrValalaLe uSerCysThr CysArgGlyS erGlyAsnLe uGlnAspGlu CysGluGlnL euGluArgSe rPheSerGln AsnProCysLeu
1101 TCGTGGAGGC CATTGCAGCT AAGATGCGTT TCCACAGACA GCTCTTCTCC CAGGACTGGG CAGACTCTAC TTTTTCAGTG GTGCAGCAGC AGAACAGCAA
AGCACCTCCG GTAACGTCGA TTCTACGCCA TTCTACGCCA AGGTGTCTGT CGAGAGAGAG GTCTGAGATG AAAAGTCAC CACGTCGTGC TCTTGTCTGT
339 ValGluAl aIleAlaala LysMetArgP heHisArgG1 nLeuPheSer GlnAspTrpA laAspSerTh rPheSerVal ValGlnGlnG InAsnSerAsn
1201 CCCTGCTCTG AGACTGCAGC CCAGGCTACC CATCTTTCT TCTCCATCC TTCCCTTGAT TCTGCTGCAG ACCCTCTGTT AGCTGGGCTT CCTCAGGGTC
GGGACGAGAC TCTGACGTCG GGTCCGATGG GTAAGAAAGA AAGAGTAGG AAGGAACTA AGACGACGTC TGGGAGACCA TCGACCCGAA GGAGTCCCAG
372 ProAlaLeu ArgLeuGlnP roArgLeuPr oIleLeuSer pheSerIleL euProLeuI1 eLeuLeuGln ThrLeuTrp
1301 CTTTGTCTC TCCACCACAC CCAGACTGAT TTGCAGCCTG TGGTGGGAGA GAACCTCGCA GCTGTGGAG GAAGACGGAG CGTGTACAC AGCAACCCGG
GAAACAGGAG AGGTGGTGTG GGTCTGACTA AACGTCGGAC ACCACCTCT TCTGAGCGGT CGGACACCTT CTTCTGCGTC GCACGATGTG TCGTTGGGCC
1401 AACCAACCAG GCATTCCGCA GCACATCCCG TCTGCTCCAG AAGAGGTCTT AGAAGTGAGG GCTGTGACCC TTCCGATCCT GAGCGGCTAG TTTTCAAAAC
TTGGTTGGTC CGTAAGGCGT CGTGTAGGC AGACGAGGTC TTCTCCAGAA TCTTCACTCC CGACACTGGG AAGGCTAGGA CTCGCCGATC AAAAGTTTGG
1501 TCCTTTGCC CTGCTTCCCT CTGGCTCAGG CTGCTCCTCC TTAGGACTTT GTGGGTCCAG TTTTGCCTTC TGTCTGTATG GTGATTAGCG GCTCACCTCC
AGGGAACGGG GACGAAGGAA GACCGAGTCC GACGAGGAGG AATCCTGAAA CACCCAGGTC AAAACGGAAG ACAAGACTAC CACTAATCGC CGAGTGGAGG
1601 AGCGCTCTT CCTGTTTCCC AGGACCAACC AGAGGCTAAG GAATCAGTCA TTCCCTGTTG CCTTCTCCAG GAAGGCAGGC TAAGGGTTCT GAGGTGACTG
TCGCGAAGAA GGACAAAGG TCCTGGTGGG TCTCCGATT CTTAGTCACT AAGGGACAAC GGAAGAGGTC CTTCCGTCGG ATTCCCAAGA CTCCACTGAC
1701 AGAAAAATG TTCTTTTGTG TGAAGGCTG GTGCTCCAGC CTCCACGTCC CTCTGAATGG AAGATAAAAA CCTGCTGGTG TCTTGACTGC TCTGCCAGGC
TCTTTTITACA AAGGAACAC ACCTTCCGAC CACGAGGTG GAGGTGCAGG GAGACTTACC TTCTATTTTTT GGACGACCAC AGAAGTACG AGACGGTCCG
1801 AATCTGAAC ATTGTTGGCAT GAAGAGCTAA AGTCTTTGGG TCTTGTTTAA CTCCTATTAC TGTCCTCCAAA TTCCCTTAGT CCCTTGGGTC ATGATTAAAC
TTAGGACTTG TAAACCCGTA CTTCTCGATT TCAGAAACCC AGAACAAAT GAGGATAATG ACAGGGGTTT AAGGGGATCA GGAACCCAG TACTAATTG
1901 ATTTTGACTT AAAAAAAA AAAAAAAA AAAAAA
TAAACTGAA TTTTTTTTTT TTTTTTTTTT TTTTTT

FIG. 1B



hGFra3 1 MVRPLNPRPLPPVVLMLLLPPSPPLAAGDPLPTESRLMNSCLQARRK
mGFra3 1 . . MGLSWSPRPPLLLMILLVLSLW.LPLGAGNSLATENRFVNSCTQARKK

hGFra3 51 CQADPTCSAAHYHLDSCTSSIISTPLPSEEPSVPAADCLEAAQQLRNSSLIG
mGFra3 48 CEANPACKAAYQHLGSCCTSSISRPLPLEESAMSAADCLEAAEQQLRNSSLID

hGFra3 101 CMCHRRMKNQVACLDIYWTVHRAARSLGN YELDVSPYEDTTSKPKWMNLS
mGFra3 98 CRCHRRMKHQATCLDIYWTVHPARSLGD YELDVSPYEDTTSKPKWMNLS

hGFra3 151 KLNMLKPDSDLCLKFAMLC TLN DKCDRLRKAYGEACSGPHCQRHVCLRQL
mGFra3 148 KLNMLKPDSDLCLKFAMLC TLH DKCDRLRKAYGEACSGIR CQRHLC LAQL

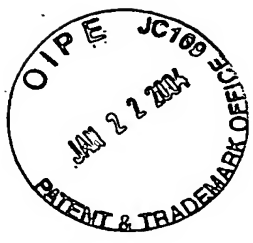
hGFra3 201 LTF FEKAAEP HAQGLLLCPCAPND RGCGERRRNTIAPNCALPVPVAPNCLE
mGFra3 198 RSF FEKAAES HAQGLLLCPCAPE D AGCGERRRNTIAPS CALP SVTPNCLD

hGFra3 251 LRRLCFSDPLCRSRLVDFQTHCHPMDILGT CATEQSRCLRAYLGLIGTAM
mGFra3 248 LRSFCRADPLCRSRLMDFQTHCHPMDILGT CATEQSRCLRAYLGLIGTAM

hGFra3 301 TPNFVSNVNTSVALSCTCRGSGN LQEECEMLEGFFSHNPCLTEAIAAKMR
mGFra3 298 TPNFISKVNTTVALSCTCRGSGN LQDECEQLERSFSQNPCLVEAIAAKMR

hGFra3 351 FHSQLFSQDWPHPPTFAVMAHQNENPAVRPQPWVPSLFSC TLP LILL LSLW
mGFra3 348 FHRQLFSQDWA DSTFSV VQQQNSNPA LRLQPRLPILSFSI LPLILL QTLW

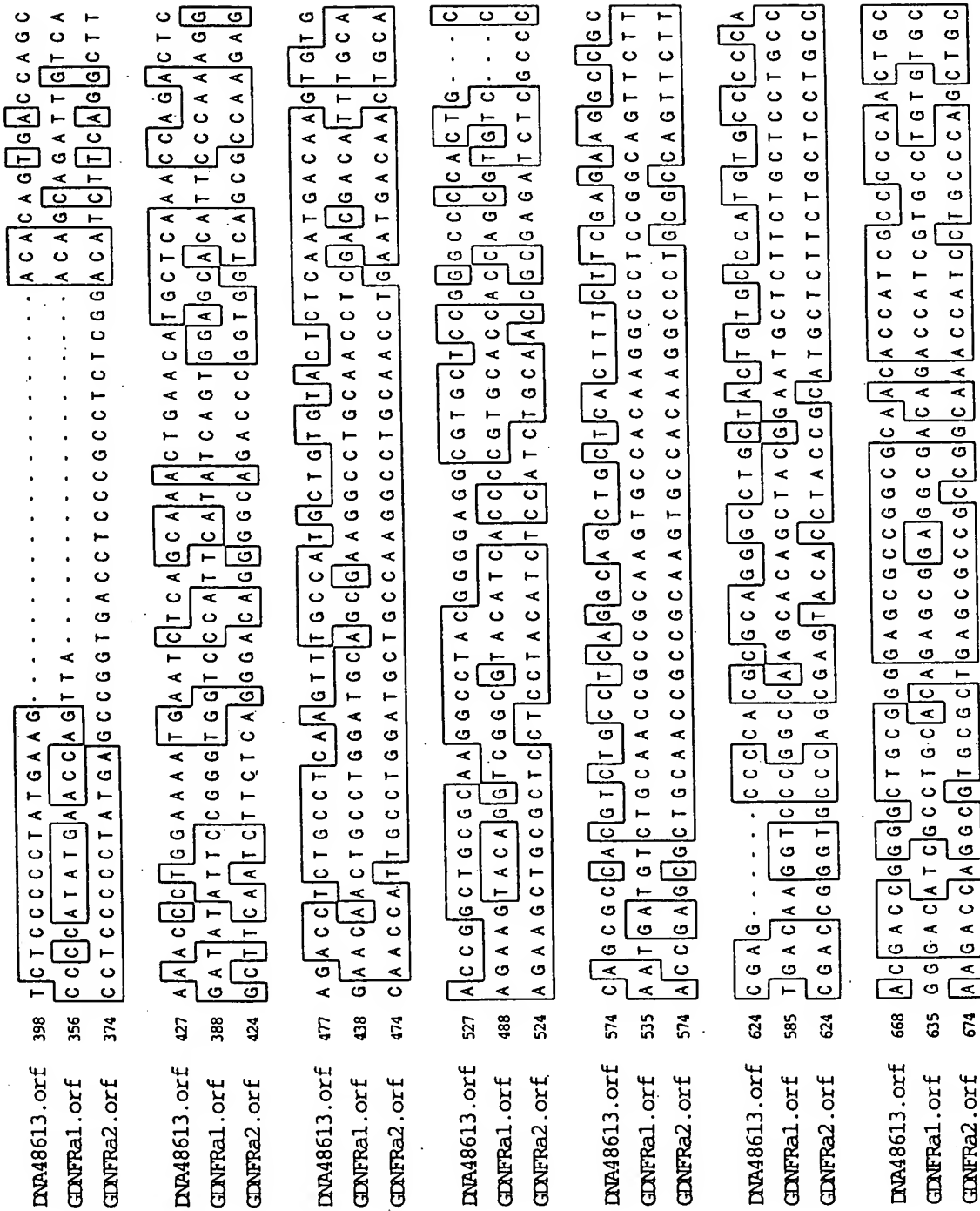
FIG. 3



48613	1	MVRPLNPRPLPPVVLMLLLLPSPPLPLAAGDPLPTESRLMNSCLQARRK
48614	1	MVRPLNPRPLPPVVLMLLLLPSPPLPLAAGDPLPTESRLMNSCLQARRK
48613	51	CQADPTCSAAYYHHLDSCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG
48614	51	CQADPTCSAAYYHHLDSCTSSISTPLPSEEPSVPADCLEAAQQLRNSSLIG
48613	101	CMCHRRMKNQVACLDIYWTVHRRARSLGNYELDVSPYEDTVTSKPWKMNLS
48614	101	CMCHRRMKNQVACLDIYWTVHRRARSL.....
48613	151	KLNMLKPPDSDLCLKFAMLCCTLNDKCDRLRKAYGEACSGPHCQRHVCLRQL
48614	127DSDLCLKFAMLCCTLNDKCDRLRKAYGEACSGPHCQRHVCLRQL
48613	201	LTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE
48614	170	LTFFEKAAEPHAQGLLLCPCAPNDRGCGERRRNTIAPNCALPPVAPNCLE
48613	251	LRRLCFSDPLCRSRLVDFQTHCH.PMDILGTCATEQSRCLRAYLGLIGTAM
48614	220	LRRLCFSDPLCRSRLVDFQTHCH.PMDILGTCATEQSRCLRAYLGLIGTAM
48613	301	TPNFVSNVNTSVALSCTCRSGNMQEECEMLEGFFFSHNPCLTEAIAAKMR
48614	270	TPNFVSNVNTSVALSCTCRSGNMQEECEMLEGFFFSHNPCLTEAIAAKMR
48613	351	FHSQLFSQDWPHPPTFAVMAHQENENPAVRPQPWPVPSLFSCTLPLILLSLW
48614	320	FHSQLFSQDWPHPPTFAVMAHQENENPAVRPQPWPVPSLFSCTLPLILLSLW

FIG. 4

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DNA48613.orf	718	G	C	G	C	T	G	C	C	...	G	C	C	T	G	T	G	G	C	C	C	A	A	C	T	G	C	C	T	G	G	A	G	C	T	G	C	G	C	T	C	T	G						
GINFral1.orf	685	T	C	C	T	A	T	G	A	A	G	A	G	C	C	A	A	C	T	G	T	T	G	A	A	T	T	G	C	A	G	G	A	C	T	C	C	T	G										
GINFral2.orf	724	T	C	C	T	A	T	G	A	G	G	A	A	G	C	C	A	A	C	T	G	C	T	G	G	A	C	T	G	C	G	T	G	C	G	T	G	C	G	T	G	T	G						
DNA48613.orf	765	C	T	T	C	T	C	G	A	C	C	C	G	C	T	T	T	G	C	A	G	A	T	C	A	G	A	T	T	C	A	G	A	T	T	C	C	A	A	C	T								
GINFral1.orf	735	C	A	A	G	A	C	G	A	A	T	T	A	C	A	T	C	T	G	C	A	G	A	T	C	T	G	C	C	T	T	G	C	G	A	T	T	T	T	A	C	C	A	C	T				
GINFral2.orf	774	C	C	G	G	A	C	T	G	A	C	C	A	C	T	G	T	C	G	G	T	C	C	G	C	G	A	C	T	T	C	C	A	T	T	C	C	A	T	T	G	C	C	A	A	T			
DNA48613.orf	815	G	C	C	A	T	C	C	C	A	T	G	G	A	C	A	T	T	G	T	G	C	A	A	C	A	G	A	G	C	A	G	T	C	A	G	A	G	T	C	A	G	A	...					
GINFral1.orf	785	G	C	C	A	G	C	C	A	G	A	G	T	C	A	A	G	T	C	T	G	T	C	A	G	C	A	G	C	T	T	A	A	G	A	A	A	A	A	C	T	A	C	G	C	T			
GINFral2.orf	824	G	T	C	G	A	G	C	T	C	C	T	A	C	A	G	A	C	G	T	C	A	C	C	A	G	C	T	G	C	C	T	G	C	G	A	C	A	A	T	T	A	C	C	A	G			
DNA48613.orf	862	...	T	G	T	C	T	A	C	G	A	G	C	A	T	A	C	C	T	G	G	G	C	T	G	A	T	T	G	G	A	C	T	G	C	C	A	T	G	A	C	C	C	C	A	A			
GINFral1.orf	835	G	A	C	T	G	C	C	T	C	T	C	G	C	C	T	A	C	T	C	G	G	G	C	T	A	T	T	G	G	C	A	C	A	G	T	C	A	T	G	A	C	C	C	C	A	A		
GINFral2.orf	874	G	C	G	T	G	T	C	T	G	G	G	C	T	C	T	A	T	G	C	T	G	G	C	A	T	G	A	T	T	G	G	T	T	G	A	C	A	T	G	A	C	A	C	C	T	A	A	
DNA48613.orf	909	C	T	T	G	T	C	A	G	C	A	A	T	G	T	C	A	...	A	C	A	C	A	G	T	G	C	C	T	T	A	A	G	C	T	G	C	A	C	C	T								
GINFral1.orf	885	C	T	A	C	A	T	A	G	A	C	T	C	C	A	G	T	A	...	G	C	C	T	C	A	G	T	G	C	C	C	C	C	A	T	G	G	T	G	T	G	A	C	T					
GINFral2.orf	924	C	T	A	T	G	T	G	G	A	C	T	C	C	A	G	C	C	C	A	C	T	G	G	C	A	T	C	G	T	G	T	G	T	C	C	C	C	T	G	G	T	G	C	A	G	C	T	
DNA48613.orf	953	G	C	C	G	A	G	G	C	A	G	T	G	G	C	A	A	C	C	T	G	C	A	G	G	A	G	T	G	T	G	A	A	A	T	G	C	T	G	G	A	A	G	G	T	T	C		
GINFral1.orf	929	G	C	A	G	C	A	C	A	G	T	G	G	G	A	A	C	G	A	C	C	T	A	G	A	A	G	A	G	T	G	C	T	T	G	A	A	A	T	T	C	T	T	G	A	A	T	T	C
GINFral2.orf	974	G	T	C	G	T	G	C	A	G	C	G	G	G	A	A	C	A	T	G	A	G	G	A	G	T	G	T	G	A	G	A	G	T	T	C	T	C	A	G	G	G	A	C					
DNA48613.orf	1003	T	T	C	T	C	C	A	C	A	A	C	C	C	C	T	T	G	C	C	T	C	A	C	G	G	A	G	C	C	A	T	T	G	C	A	G	C	T	A	A	G	A	T	G	C	G	T	T
GINFral1.orf	979	T	T	C	A	G	G	A	C	A	A	T	A	C	A	T	G	T	C	T	T	A	A	A	A	T	G	C	A	T	T	C	A	A	G	C	C	T	T	T	G	G	C	A	A	T	G	G	
GINFral2.orf	1024	T	T	C	A	C	C	G	A	G	A	C	C	C	A	T	G	C	C	T	C	C	G	A	A	C	G	C	C	A	T	C	C	A	G	C	C	T	T	T	G	G	C	A	A	C	G	G	

FIG. 5C

DNA48613.orf 1053 T C A C A G C C A A C T C T T C T C C C A G G A C T G G C C A C A C C C T A C C T T T G C T G T G A
GINFRa1.orf 1029 C T C C G A T G T G A C C G T G T G G C A G C C A G C C T T C C C A G T A C A G A C C A C C A C T G
GINFRa2.orf 1074 A C G G A C G T G A A C G T G T C C C C A A A A G G C C C C T C G T T C C A G G C C A C C C A G G

DNA48613.orf 1103 T G G C A C A C A G A T G A A A C C C T G C T G T G A G G C C A C A G C C T G G T G C C C
GINFRa1.orf 1079 C C A C T A C C A C C A C T G C C C T C G G G T T A A G A A C A A A C C C C T G G G C C A G C A
GINFRa2.orf 1124 C C C C T C G G G T G G A G A G A C G C C T T C T T T G C C A G A T G A C C T C A G T G A C A G T

DNA48613.orf 1153 T C T C T T T C T C C T G C A C G C T T C C C T T G A T T C T G C T C C T G A G C C T A T G G T A
GINFRa1.orf 1129 G G G T C T G A G A A T G A A T T C C C A C T C A T G T T T G C C A C C G T G T G C A A A T T T
GINFRa2.orf 1174 A C C A G C T T G G G G A C C A G T G T C A T C A C C A C C T G C A C G T C T G T C C A G G A G C A

DNA48613.orf 1203 G
GINFRa1.orf 1179 A C A G G C A C A G A A G C T G A A T C C A A T G T G T C G G G C A A T A C A C A C C T C T G T A
GINFRa2.orf 1224 G G G G C T G A A G G C C A C A A C T C C A A A G A G T A A G C A T G T G C T T C A C A G A G C

GINFRa1.orf 1229 T T T C C A A T G G T A A T T A T G A A A A G A A G G T C T C G T G C T T C C A G C C A C A T A
GINFRa2.orf 1274 T C A C G A C A A A T A T C A T C C C A G G G A G T A A C A A G G T G A T C A A A C C T A A C T C A

GINFRa1.orf 1279 A C C A C A A A A T C A A T G G C T G C T C C A A G C T G T G G T C T G A G C C C A C T G C T
GINFRa2.orf 1324 G G C C C C A G C A G A G C C A G A C C G T C G G C T G C C T T G A C C C G T G C T G T C T C C T

GINFRa1.orf 1329 G G T C C T G T G G T A A C C G C T C T G T C C A C C C T A T T A T C T T A A C A G A A C A T
GINFRa2.orf 1374 G A T G C T G A A C A G G C C T T G T A G
GINFRa1.orf 1379 C A T A G

FIG. 5D



DNA48613 1 MVRPLNPRPLPPVVLMLLLLLPSPPLPLAAGDPLPTESRLMNSCLQARRK
GDNFrac1 1 MFLAT--LYFALL-PLLDLLLSA--EVSGGD--RL--DCVKASDQ
GDNFrac2 1 MILANVFCLFFFLDET LRS LASPS--SLQGPELHGWRPPV--DCVRANEL

DNA48613 51 CQADPTCSAAYHHLDSC TSSISTPLP-SEEPSVPADCLEAAQQLRNSSLI
GDNFrac1 36 CLKEQSCSTKYRTL RQCVAGKETN FSLASGLEAKDECRSAMEAL KQKSLY
GDNFrac2 47 CAAESNCSSRYRTL RQCLAGRDNRN--TMLANK ECAAL EVLQESPLY

DNA48613 100 GCMCHRRRMKNQVA CLDIYWTVHRRARSLGNYELDVSPYEDT VTSKPWKMN L
GDNFrac1 86 NCRCKRGMKKEKNCLRIYWSMYQSL-QGNOLL EDSPYEPVNSRLSDIFRV
GDNFrac2 92 DCRCKRGMKKELOCLQIYWSIHLGLTEGE E FYEASPYEPVT SRLSDIFRL

DNA48613 150 SKL-----NMLKPOS DLCLKFAMLCTLNDKCDRLRKAYGEACS-----
GDNFrac1 135 VPFIS--VEHI--PKGN NCLDAAKACNLDDICKKYRSAYITPCTTSVS-
GDNFrac2 142 ASIFS GTGADPVVSAKSNHCLDAAKACNLNDNCKKLRS SYISICNREIS P

DNA48613 188 GPHCORHVC L RQLLTFFEKAAEPHAQGLLLCP CAPNDRGCGERRRNTIAP
GDNFrac1 179 NDVCNRRKCHKALRQFFDKVPAKHSYGMLFCSC--RDI ACTERRRQTIVP
GDNFrac2 192 TERCNRRKCHKALRQFFDRVPSEYTYRMLFCSC--QDQACAERRRQTILP

DNA48613 238 NCALPPVA-PNCLELRRLCFSDPLCRSRLVDFQTHCHP-MDILGT CATEQ
GDNFrac1 227 VCSYEEREKPNCLNLQDSCKTNYICRSRLADFFTNCOPESSRSVSSCLKEN
GDNFrac2 240 SCSYEDKEKPNCLDLRGVCR TDHLCRSRLADFHANCRASYQVTSCPADN

DNA48613 286 -SRCLRAYLGLIGTAMTPNFVSNV--NTSVALSCTCRGSGN LQEECEMLE
GDNFrac1 277 YADCLLAYSGLIGTVMTPNYIDSS--SLSVAPWCD CSNSGNDLEECLKFL
GDNFrac2 290 YQACLGSYAGMIGFDMTPNYVDSSPTGIVVSPWCS CRGSGNMEECEKFL

DNA48613 333 GFFSHNPCLTEAIAA-----KMR FHSOLF S
GDNFrac1 325 NFFKDN T CLKNAIQAFNGS DVTVWOPAFPVQT TATT T TALRVKNKPLG
GDNFrac2 340 R DFTENPCLRNAIQAFNGT D VNVSPKGPSFQATQAPRVEK T PSLPDDL S

DNA48613 358 Q-----DWPHPPTFAVMAHONENPAVRPO-----
GDNFrac1 375 PAGSENEIPTHVLP PCANLQAQKLKSNVSGNTHLCISNGNYEKEGLGASS
GDNFrac2 390 OSTSL--LGTSVIT TCTSVQEQGLKANNSKELSM CFT--ELTTNIIPGSN

DNA48613 381 ----PWVPSLFSCTLP L I L L L S L W-----
GDNFrac1 425 HITTKSMAAPP SCGLSPLLVLVVTALSTLLSLTETS
GDNFrac2 435 KVIK P NSGPSRARPSAALT VLSVLM LKQAL-----

FIG. 6

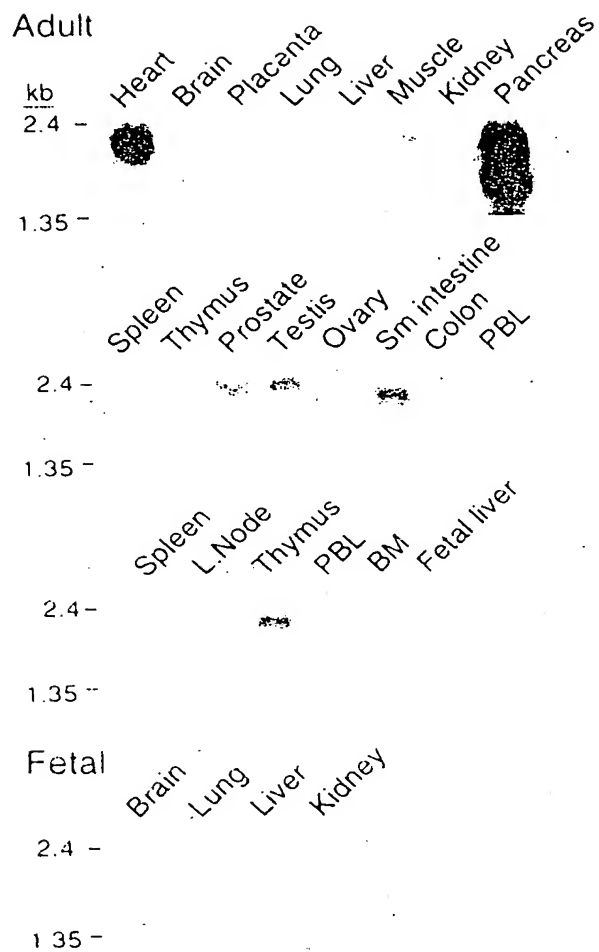


FIG. 7

GFR α 3

GFR α 2

GFR α 1

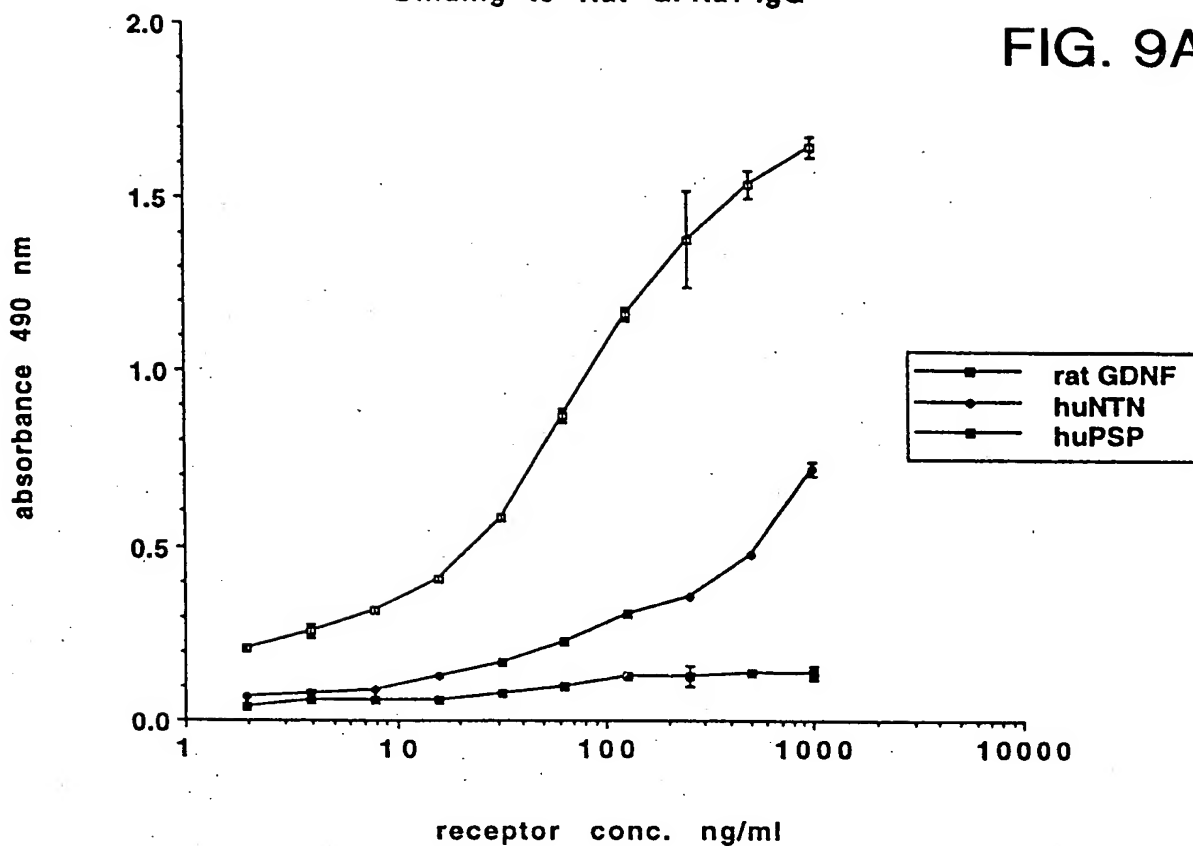


FIG. 8



Binding to Rat GFRa1-IgG

FIG. 9A



Binding to Human GFRa2-IgG

FIG. 9B

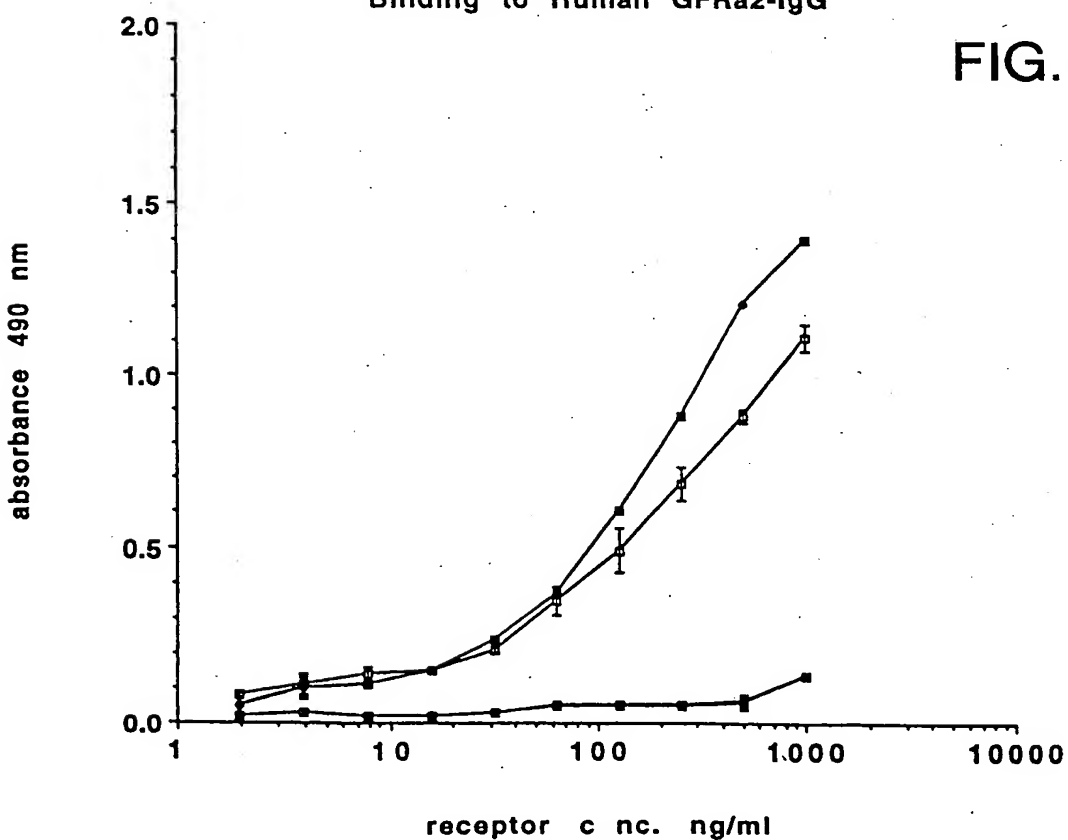


FIG. 10

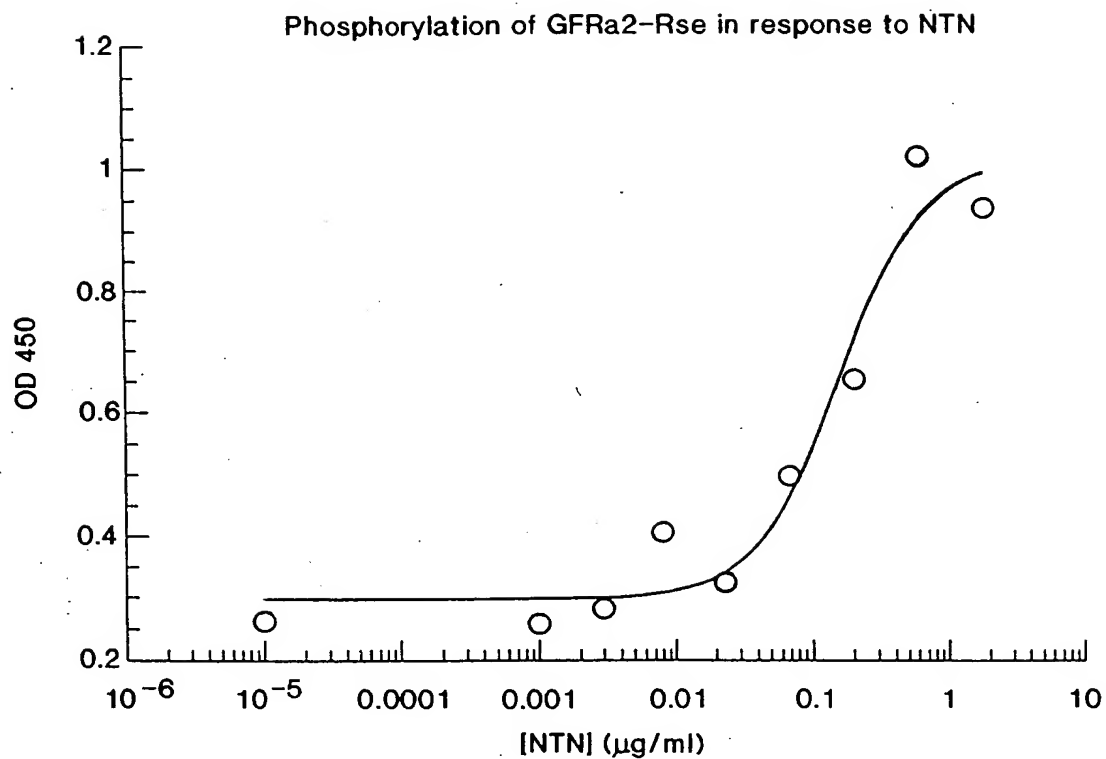
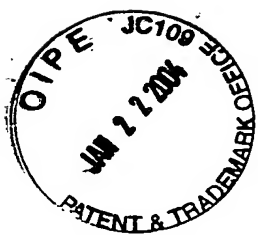


FIG. 11

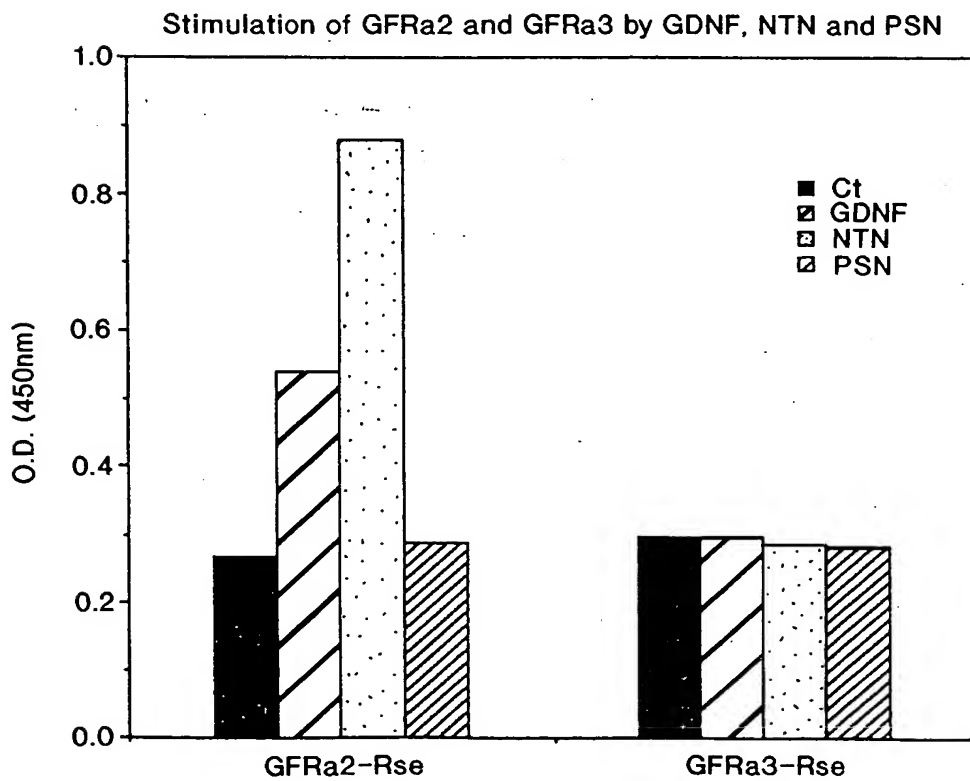


FIG. 12

Agonistic activity of anti gD mAbs in gD-alpha2-rse KIRA

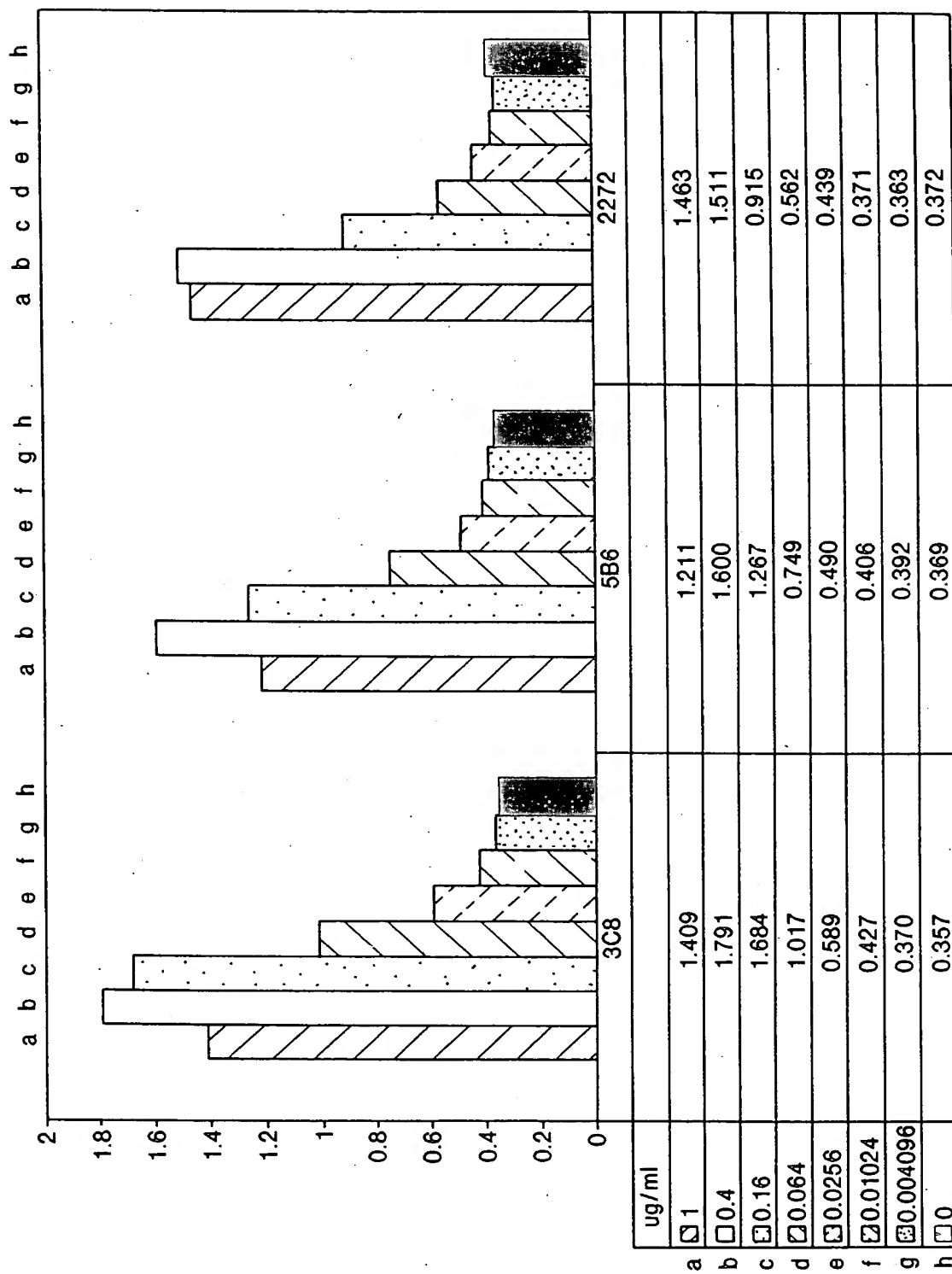


FIG. 13